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<!--StartFragment-->RESULT 5
AAM49641
ID      AAM49641 standard; protein; 836 AA.
XX
AC      AAM49641;
XX
DT      17-MAY-2002 (first entry)
XX
DE      Human tumour-associated antigen B345 protein SEQ ID NO 4.
XX
KW      Tumour-associated antigen; human; B345; cytostatic; cell communication;
KW      cell interaction; signal transduction; metastasis; cancer; colon;
KW      immunotherapy; carcinoma; lung; diagnosis.
XX
OS      Homo sapiens.
XX
PN      WO200204508-A1.
XX
PD      17-JAN-2002.
XX
PF      05-JUL-2001; 2001WO-EP007705.
XX
PR      07-JUL-2000; 2000DE-01033080.
PR      19-APR-2001; 2001DE-01019294.
XX
PA      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI      Schweifer N, Scherl-Mostageer M, Sommergruber W, Abseher R;
XX
DR      WPI; 2002-171704/22.
DR      N-PSDB; ABA99507.
XX
PT      New tumor-associated antigen B345, useful for diagnosis and immunotherapy
PT      of tumors, also related nucleic acid and antibodies.
XX
PS      Claim 1; Page 85-88; 102pp; German.
XX
CC      This invention describes a novel tumour-associated antigen, designated
CC      B345 which has cytostatic activity. B345 is involved in communication,
CC      interaction and/or signal transduction with extracellular components and
CC      ligands, especially in the metastatic potential of cancers, particularly
CC      of the colon. B345 or its immunogenic fragments, also the DNA that
CC      encodes it, are useful for immunotherapy of cancer, particularly
CC      carcinoma of lung or colon. Antibodies raised against B345 are useful for
CC      treatment and diagnosis of cancers that are associated with B345
CC      expression, including their use for targeted delivery of cytotoxic or
CC      radioactive agents. Probes derived from B345 can be used to detect tumour
CC      -specific mutations in the B345 sequence, and can be used to screen for
CC      B345 specific modulators. This sequence represents a human B345 tumour-
CC      associated antigen described in the invention
XX
SQ      Sequence 836 AA;

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Query Match          99.8%; Score 4385; DB 5; Length 836;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 834; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MAGLNCVGSIALLGVLVLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLAKPCYIVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MAGLNCVGSIALLGVLVLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLAKPCYIVI 60

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Qy	61	SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGSPCPFGEVQLQPSTSLIPT	120
Db	61	SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGSPCPFGEVQLQPSTSLIPT	120
Qy	121	LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPOGVTHSISGRIDATVVRIGTFCSN	180
Db	121	LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPOGVTHSISGRIDATVVRIGTFCSN	180
Qy	181	GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY	240
Db	181	GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY	240
Qy	241	PEGFPPEDELMTWQFVPAHLRASVSFLNFNLSNCERKEERVEYIIPGSTTNPEVFKLEDK	300
Db	241	PEGFPPEDELMTWQFVPAHLRASVSFLNFNLSNCERKEERVEYIIPGSTTNPEVFKLEDK	300
Qy	301	QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHPQONESNKIYVVDLSNERAMSLTIE	360
Db	301	QPGNMAGNFNLSLQGCDDAQSPGILRLQFQVLVQHPQONESNKIYVVDLSNERAMSLTIE	360
Qy	361	PRPVKQSRKFVPGCFVCLESRTCCSNLTLSGSKHKISFLCDDLRLMMNVKTIISCTDH	420
Db	361	PRPVKQSRKFVPGCFVCLESRTCCSNLTLSGSKHKISFLCDDLRLMMNVKTIISCTDH	420
Qy	421	RYCQRKSYSLOVPSDILHLPVELHDFSMKLLVPKDRLSLVLPQAQLQOHTHEKPCNTSF	480
Db	421	RYCQRKSYSLOVPSDILHLPVELHDFSMKLLVPKDRLSLVLPQAQLQOHTHEKPCNTSF	480
Qy	481	SYLVASAIPSQDLYFGSFCPGSGIKQIQVKQNISVTLRTFAPSFRQEASRQLTVSFIPI	540
Db	481	SYLVASAIPSQDLYFGSFCPGSGIKQIQVKQNISVTLRTFAPSFRQEASRQLTVSFIPI	540
Qy	541	FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSMNISVPRDQVACLTFKERSGVVQC	600
Db	541	FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSMNISVPRDQVACLTFKERSGVVQC	600
Qy	601	TGRAFMIIQEQRTAAEEIFSLDEDVLPKPSFHHHSFWVNIISNCSPSTSGKQLDLLFSVTLT	660
Db	601	TGRAFMIIQEQRTAAEEIFSLDEDVLPKPSFHHHSFWVNIISNCSPSTSGKQLDLLFSVTLT	660
Qy	661	PRTVDLTVILIAAVGGVLLLSALGLIICCVKKKKKTKNGPAVGVIYNGNINTEMPRQPK	720
Db	661	PRTVDLTVILIAAVGGVLLLSALGLIICCVKKKKKTKNGPAVGVIYNGNINTEMPRQPK	720
Qy	721	KFKQGRKNDNSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPSPPTIC	780
Db	721	KFKQGRKNDNSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPSPPTIC	780
Qy	781	SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDDIPLLTQEPMEPAE	836
Db	781	SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDDIPLLTQEPMEPAE	836

&lt;!--EndFragment--&gt;